

## Claims

1. (~~Thrice-fourth time~~ Amended) A process for the production of a transgenic plant the seeds of which comprise an embryo exhibiting a modified cotyledons development, wherein at least one plant cell is transformed with at least one DNA cosuppression construct comprising a nucleic acid sequence derived from the an-ASKdzethaASKdzeta (ASK $\zeta$ )-gene of group II ~~is as~~ a fragment of at least 150 base pairs corresponding to the 5' untranslated region and part of the N-terminal coding region and regenerated to a plant whose embryos exhibit modified development characterized by the development of an increased number of cotyledons
- 5
- 10 ~~the modified development.~~
2. (~~once-twice~~ amended) The process according to claim 1, wherein the nucleic acid sequence derived from an ASKdzeta ASKdzetha (ASK $\zeta$ )-gene of group II is a fragment of at least 300 base pairs corresponding to the 5' untranslated region and part of the N-terminal coding region.
3. (~~please delete claim 3~~) ~~The process according to claim 1, wherein the modified development is characterised by the development of an increased number of cotyledons.~~
4. (~~Once-twice~~ Amended) The process according to claim 1, wherein the DNA cosuppression construct is an antisense or sense construct or a construct comprising a transposable element wherein the DNA construct is capable of eliminating the expression of an endogenous ASKdzeta ASKdzetha (ASK $\zeta$ )-gene of group II.
5. Delete claim 5
6. Delete claim 6
7. (~~Once-twice~~ Amended) The process according to claim 1, wherein the nucleic acid sequence derived from ~~anthe~~ an-ASK-gene of group II is a fragment of 150 to 350 bp, corresponding to the 5'-untranslated region and a part of the N-terminal coding region of ASKdzeta ASKdzetha (ASK $\zeta$ )-gene of group II.
- 5

8. The process according to claim 1, wherein the ASK-gene is in the form of a cDNA or genomic DNA.
  9. The process according to claim 1, wherein the DNA construct comprises at least one regulatory element being operably linked to the nucleic acid sequence derived from the ASK-gene of group II and being capable of directing the expression of the nucleic acid sequence derived from the ASK-gene of group II.
- 5

10. The process according to claim 9, wherein the regulatory element is a promoter and/or enhancer, in particular the 35 S CaMV-promoter.
11. The process according to claim 1, wherein the DNA construct comprises a transcription termination signal operably linked to the nucleic acid sequences derived from the ASK-gene of group II, in particular a poly A addition site.
12. The process according to claim 1, wherein the DNA construct is cloned into a vector, in particular a plasmid or viral vector.
13. The process according to claim 1, wherein the plant cell is from a monocotyledonous or dicotyledonous plant.
14. The process according to claim 13, wherein the monocotyledonous or dicotyledonous plant is Arabidopsis, brassica, cotton, potato, soya, sugar beet, sugar cane, an ornamental plant, rice, maize, barley or wheat.
15. The process according to claim 1, wherein the plant cell is transformed by transfer of the DNA construct by a method selected from the group selected from: transfer via a bacterium, transfer via virus to the cell, transfer via direct uptake of the DNA construct by microinjection of the DNA construct, transfer via direct uptake of the DNA construct by particle bombardment.
16. The process according to claim 1, wherein the transformed cell is regenerated into a differentiated plant.
17. (Deleted)
18. (Deleted)
19. (Deleted)
20. A plant comprising at least one cell according to claim 13.
21. Seeds and plant derived tissue comprising a genetically modified cell according to claim 20.
22. (once amended)A plant produced according to the process of according-to-claim 1.

23. Seeds and plant derived tissue obtained from a plant produced by the process according to ~~according to~~ claim 1.
24. (~~Once twice~~ Amended) A transgenic *Arabidopsis* plant the seeds of which comprises an embryo exhibiting a modified cotyledons development, said plant comprising at least one plant cell transformed by a nucleic acid sequence derived from at least one ASKdzeta ~~ASKdzeta~~ (ASKζ)-gene of group II wherein at least one embryo exhibits the modified development.

Page 5, line 26

In a particularly preferred embodiment, the nucleic acid sequence derived from an ASK-gene is an ASKdzethaASKdzeta or an ASKetha gene. ASK is the abbreviation for Arabidopsis SHAGGY-related protein kinases (Dornelas et al., 1998). The cDNA and genomic DNA sequences of various ASK-gene, including the ASK-genes of group II, are published in Dornelas et al. Gene 212 (1998), 249-257 and Dornelas et al. Plant Molecular Biology 39, (1999) 137-147, whose content with respect to the sequence and its provision is fully incorporated herein by reference. This article contains the reference to Accession X94938 in the GenBank. The Arabidopsis thaliana mRNA for shaggy-like Kinase Dzeta identified as Accession X94938 is provided herein as Seq. Id. No. 6. In the context of the present invention, ASK-genes of group II are the ASK genes classified according to Dornelas et al. (199) in group II of SGG/GSK-3 homologues, in particular ASKiota, ASKdzethaASKdzeta and ASKetha. In a particularly preferred embodiment, the ASK-genes of group II of the present invention are ASKdzethaASKdzeta and ASKetha genes.

Page 6, line 3

According to the present invention, the DNA constructs, in particular the antisense and sense constructs used, comprise a nucleic acid sequence derived from an ASK-gene of group II, in particular the ASKdzethaASKdzeta and/or ASKetha gene, or parts thereof.

Page 6, line 7

In a preferred embodiment of the present invention, the use of the ASKdzethaASKdzeta gene in antisense constructs or in sense constructs used from instance in co-suppression technology (co-suppression constructs) for eliminating wild-type seeds, whose embryos and seedlings are characterized by the development of, in contrast to that of a wild-type plant, an increased number of cotyledons obviously caused, without being limited by theory, by abnormal divisions of the hypophyseal cell and abnormal development of the upper and lower tiers of the embryo. As a consequence, the embryo and seedling exhibits supernumerary cells and shows polycotyly.